

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 28, 2003, 00:58:38 ; Search time 2074 Seconds
(without alignments)
10968.655 Million cell updates/sec

Title: US-09-308-829-1

Perfect score: 936
Sequence: 1 caacctgactataatg.....gagcttacccttaatta 936

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hic:*
12: gb_estc3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102.2	10.9	1201	9	AL565455
2	91	9.7	1200	13	AL565455 AL565455
3	87	9.3	1101	29	BX437758 BX437758
4	87	9.3	1200	13	CNS0039G CNS0039G
					AL063921 Drosophila
					BX415878 BX415878

5	85.4	9.1	1101	29	CNS00EVL	AL069706 Drosophila
6	81.2	8.7	1101	29	CNS0039G	AL063921 Drosophila
7	81.2	8.7	1201	9	AL565455	AL565455 AL565455
8	80	8.5	1101	29	CNS00EVL	AL069706 Drosophila
9	79.2	8.5	1201	9	AL56104	AL56104 AL56104
10	78	8.3	1101	29	CNS0021J	AL061936 Drosophila
11	76.8	8.2	1101	29	CNS003BD	AL064091 Drosophila
12	76.4	8.2	994	29	CNS04NOJ	AL068972 Tetradon
13	75.4	8.1	1200	13	BX415878	BX415878 BX415878
14	74.2	7.9	994	13	BX414650	BX414650 BX414650
15	73.2	7.8	1201	13	BX439779	BX439779 BX439779
16	72.6	7.6	836	29	CNS01100	AL099642 Drosophila
17	71.4	7.6	1201	9	AL56104	AL56104 AL56104
18	70.2	7.5	1010	14	CD171719	CD171719 AGENCOURT
19	70.2	7.5	1200	13	BX437739	BX437739 BX437739
20	70	7.5	795	29	AG044101	AG044101 Pan trogl
21	70	7.5	1124	13	BX436282	BX436282 BX436282
22	69.8	7.4	1101	29	CNS00E07	AL069440 Drosophila
23	69.6	7.4	1045	13	BX456814	BX456814 BX456814
24	69.6	7.4	1201	13	BX366070	BX366070 BX366070
25	69.4	7.4	1092	29	CNS020K7	AL175696 Tetradon
26	69.2	7.4	829	29	CNS03LUB	AL249932 Tetradon
27	69.2	7.4	1202	29	CC262481	CC262481 CH261-167
28	69	7.4	1008	14	CD329035	CD329035 AGENCOURT
29	68.8	7.4	1200	13	BX437758	BX437758 BX437758
30	68.6	7.3	994	13	BX436885	BX436885 BX436885
31	68.6	7.3	1098	13	BX377526	BX377526 BX377526
32	68.6	7.3	1165	13	BX38369	BX38369 BX38369
33	68.4	7.3	1056	13	BX415058	BX415058 BX415058
34	68.2	7.3	956	13	BX414969	BX414969 BX414969
35	68.2	7.3	1101	29	CNS003DQ	AL064580 Drosophila
36	68	7.3	1201	13	BX406288	BX406288 BX406288
37	67.8	7.2	1225	29	CNS0161D	AL106171 Drosophila
38	67.4	7.2	1098	13	BX377526	BX377526 BX377526
39	67.2	7.2	939	14	BY720774	BY720774 BY720774
40	67.2	7.2	1201	13	BX360780	BX360780 BX360780
41	67.2	7.2	1201	13	BX461824	BX461824 BX461824
42	67	7.2	928	29	CNS00DKY	AL071865 Drosophila
43	66.8	7.1	949	14	CA465606	CA465606 AGENCOURT
44	66.6	7.1	876	29	CNS00991	AL053529 Drosophila
45	66.6	7.1	1201	13	BX443774	BX443774 BX443774

ALIGNMENTS

RESULT 1
AL565455
LOCUS
DEFINITION
AL565455 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF005YO18 3-PRIME, mRNA sequence.
ACCESSION
AL565455
VERSION
AL565455.2 GI:30549492
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On Feb 16, 2001 this sequence version replaced gi:12916848.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by life technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9232.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DF005BH09NP1&cluster=9232.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

Db	582	GAMKATWTTT	KTTTAT	WMKRAGACATWTTT	TTTTTT	WTMAARGMKMTWTT	TTTTTT	TWT	641
OY	455	TATTTTATATCT	TAAATTC	CACCGGTGAGT	ACATCTATG	GAGAAATTA	CGCTGCTC	514	
Db	642	TTTTTTTTT	GTGTTT	WWWDRGAR	FRKAKAT	KWTTT	WTWMT	AVAMAGAA	RRKRATWTTWA
OY	515	AAATTAATTAAG	TAATCAT	TAAATTAAT	TGGAATTC	ATATTAAT	TATTTGCG	GAAATCTCAAC	574
Db	702	AAMWMMW	GAARAGAA	GAGAAATWTTT	TTTTTT	ATYKAGAR	GATWTT	----	AMAWMTATRA
OY	575	AGACCTTAAT	TAACAGAT	TTATCT	TAGAAAGAT	ATGCTAT	CTTCAGAGAA	TTTACT	634
Db	756	RGAGGAD	TTTTTT	TATWMT	TATTTTTT	WMAAGAT	BDRAAAA	MMWMTT	WTWTAAAAAAAT
OY	635	TTAAATTC	GAAAAAT	ACCTTA	TGATATTA	TAAAAATTA	TATGAC	GCTACTT	CTCTATG
Db	816	WMWAGAR	AAAAAT	WTWMAAAAA	AAAAAA	WPRBAAAT	ATATATWTT	TATATAT	---
OY	695	TAACGGC	GAGAT	TGCAAT	TGCGC	CAAAAGT	TGGAAACAT	GACCAAT	ATAGACTTAT
Db	873	AAAAAT	TAATAA	RAARAR	RMGAAAA	AAAAAT	AAAAA	MMWTT	WTATAAAAAA
OY	755	ACTACCA	AAAT	TGAAG	AGACT	TGATATTT	TTCG	CAAAAT	TATAAAGAT
Db	933	WMRAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA	AAAA
OY	815	TCAAT	TATG	AGAC	TTAGT	TAGTTC	TATGAT	TTATTC	TATG
Db	993	TWTNA	RAAAA	AAAA	MMWDTT	TATAT	WTATW	TATAG	MAAATAT
OY	875	AAAAA	CCGCC	CAAT	TATCT	GACCG	TTTTG	CTTTA	911
Db	1053	AGAWAT	KAD	GAGAT	TAATA	MTTTTT	TTTTTT	TTWTA	1089

RESULT 3

CNS0039G

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS0039G

1101 bp

DNA

GSS 03-JUN-1999

Drosophila melanogaster genome survey sequence TE3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063921

AL063921.1

GI:4941778

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephyridroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999)

Genoscope - Centre National de Sequencage

BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org>

The BDGP Drosophila BAC library was prepared by Kazutoyo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1..1101

/organism="Drosophila melanogaster"

FEATURES

Source

[illegible]

REFERENCE 1 (bases 1 to 1200)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr; Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. Contact: Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID: CS0CAP008BE020P1.
 Location/Qualifiers
 1..1200

FEATURES
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /clone="CS0CAP008104"
 /tissue="tissue="THYMUS"
 /clone_lib="Homo sapiens THYMUS"
 /note="Vector: pCMVSPORT-6; 1st strand cDNA was primed
 with a NotI-oligo(dT) primer. Five prime end enriched,
 double-strand cDNA was digested with Not I and cloned into
 the Not I and EcoRV sites of the pCMVSPORT 6 vector.
 Library was not normalized."
 BASE COUNT
 428 a 70 c 85 g 447 t 170 others

Query Match 9.3%; Score 87; DB 13; Length 1200;
 Best Local Similarity 37.4%; Pred. No. 0.0088;
 Matches 290; Conservative 110; Mismatches 366; Indels 9; Gaps 4;

41 TAAATATTAATCACTTTAATAATTTCTAATAACAGAAATCGATTTTAACTACTT 100
 1157 WATWKKMTAAATTAATTTTATTTATATWMAAATAATWTAATTTATWTAATA 1098
 101 ACTGATTTCAATGATTCCTCGACAGAAATACATTTA-ATTAGAGAAATAATGAAA 159
 1097 AAATATTATWATWATWTAATAATTTTAAATATATATWMAAATAATWTAATAAAT 1038
 160 AAGATTAACATCATCAAAATAGTTTTCATTAATTAACAGTACATGATTTCTACTTATTC 219
 1037 AATTTTTTTTTTAMWMAAATAATWTAATAATWTAATAATWTAATAATWTAATA 978
 220 ACCTATCATCAAGAGCTAAGAGACATTTGCAATGTTAAAGTGAATTAATCTTAT 279
 977 TTTTATWMTWMAAATTTTATTTTATTTATTTTATTTTAAAAAATTTAAATTTA 918
 280 GCATA--CACTATTAAGTCTTATGATTATTAAGATTCGAGGTAATTTTCAAGACA 336
 917 AAATTAATTAATAAATAAATTTTSTAATTTTATTAATTAATWTAATAATTAATA 858
 337 CACACATTAACATGATGATCTCAAAAATATAGAGGGAAGACTATTAATTAATGTCGAA 396
 857 AATTTTTTTTTTAAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 798
 397 ATGCTTATAGAGGCTCTCAAAATTTAAACGAGATGATGATGATTTTGGATTA 456
 797 ATTWMAAATAATTTATWTAATAATTTATTTATGHTATATATATNTATGATTAATA 738
 457 TTTTATATCTTATATCTCAACACCGGTGATCATCTATGAGGAATTAACCGCTCTCA 516
 737 TTTCTTTTAAAAAATWMAATWTAATAATTTATTAATTAATTAATTAATTAATA 678
 517 AATTAATTAAGTAATCAATTAATTTATTTGGAAATCAATTTATTTGGGAATCTCAACG 576
 677 AAATATATWMTWMTWTAATTAATTTATTAATTTATTAATAAATWTAATAAAT 618
 577 AACTTAATTAACAGATT---ATTCTAGAAAGATTCGTAATCTTCGAGGAATTCGAC 633
 617 AAAAAAATAAATAAATAAATWTTWMAAATAAATAAATWTTWTTTAAAAAATAT 558
 634 TTTAAATACAGAAATACCTT-ATGATTAATTAATAATTTATGACGCTACTCTCCTT 691

Db 557 TTAATAAATAATWTTTATTTTAAATTAATAAATAATWTAATAATTTTAAATTA 498
 Qy 692 ATGAACGGCAGCAATGCAATGCGCAAAAGATGCGAAACATGCAAAATGACTTAT 751
 Db 497 AAATAATTTTAAAAAATAATTAATWTAATAATTTATTAATAAATAATTAATTA 438
 Qy 752 TTGACCTACCAATGTAAGGACTGATCATGATATTTTTCGAATATATAAGATA 806
 Db 437 AAATTTTAAAGSAAASATGCDWAAATWTAAGHTTTTKDMAAAAAAAMMMMH 383

RESULT 5
 CDS00EVL 1101 bp DNA linear GSS 04-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
 DEFINITION BAC29823 of RP11-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL069706 GI:4949849
 GSS...
 ACCESSION AL069706.1
 VERSION 1
 KEYWORDS Drosophila melanogaster (fruit fly)
 SOURCE Drosophila melanogaster
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 I (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage;
 BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
 - Web: www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazuo Osoegawa and
 Aaron Mosmoser in Pletier de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RP11-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 P1 and EST libraries. A more detailed description of the BDGP's
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
 Location/Qualifiers
 1..1101

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

FEATURES
 source
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR29823"
 /clone_lib="RP11-98"
 /note="end: 17"
 Location/Qualifiers
 1..1101

BASE COUNT
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 Best Local Similarity 38.6%; Pred. No. 0.0016;
 Matches 208; Conservative 82; Mismatches 243; Indels 6; Gaps 2;
 2 AACCTGACTATTTAAATGAGCTGCACTCTTAATAAATTAATTAATTAATTAATA 61
 Db 568 AAATTTAAATAATTTATTAATTTATTAATTTATTAATTTATTAATTTATTAATTT 627
 Qy 62 AAATTTCTAAATAAAGCAATTCGATTTTAACTACTTACTGATTTCAATGATCTC 121
 Db 628 AAATTTTAAATAATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 682
 Qy 122 GTACGAGTAATACATTTTAAAGAGAGAAATAATGAATAATTAACATCATCAATAG 181
 Db 683 TWAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 742

Oy		182	TTTTTCATTAATTAGCGTATCTGTTGTCTACTCTTTTCACCTATCATCAAGAAGTACTCTA	241
Db		743	WAAATWAMWAADATATWMAATATATATWTWTAWWATAWMAWWWMTATATAMATWAMAAMAW	802
Oy		242	AGAAAGACATTTCCAAATGGTTAAAAGTAGTATCTTACTTGATCATACTATACCTCTATG	301
Db		803	AATATTAATATAMAT - AATATWAAAAAAMANAATWMAATATATATWMAAATANMAAAAAATWTAT	861
Oy		302	ATTATTAAGATTCGACGGTAAATTTTTCACGACACACATTAACATTGANTCTCAAA	361
Db		862	ATWATATATATAWMAAAAAATAMATWMTWTTTWWMAWATATAAAMAWATWMAAAAAA	921
Oy		362	AATATAGGGAAGACATATATTTTGTGCCGAATAGCTTATAGAGCCCTCCAAAAAT	421
Db		922	AAAAAAAAAATPAAAMMMWTATATTTTATTAATTAAMTATWMAATTTWMAWMTATATAT	981
Oy		422	TTPAACAGATGATCATGTAGATGTTTGGATTATTTTATATTTCTTAATCTCACACC	481
Db		982	TWTATWATATATATWMTATWATAATATATTTTATTAAMWTATATTTTMAAAAMATATATAT	1041
Oy		482	GTGAGTACATCTATGGAGAAATTACGCCTGCTCAAATAATTAAGTAAATCATATATTA	540
Db		1042	TAMWWTAMATATWMAWMAATTTWTTATATATATWTAAMATAWMAAAAAAAMAWMATWMA	1100
RESULT 6				
CNS00396/c				
LOCUS	CNS00396	1101 bp	DNA	linear GSS 03-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence Tet3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.			
ACCESSION	AL063921			
VERSION	AI063921.1	GI:9941778		
KEYWORDS	GSS.			
SOURCE	Drosophila melanogaster (fruit fly)			
ORGANISM	Drosophila melanogaster			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.			
REFERENCE	1 (bases 1 to 1101) Genoscope.			
AUTHORS	Direct Submission			
JOURNAL	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)			
COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACS. For further information please see http://www.fruitfly.org/The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oseguwa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.			
FEATURES	Location/Qualifiers			
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	/mol_type="genomic DNA"			
	/db_xref="taxon:7227"			
	/clone="BACR08K10"			
	/clone_id="RPCI-98"			
	/note="end : Tet3"			
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ORIGIN				
Query Match	8.7%, Score 81.2; DB 29; Length 1101;			

	Best Local Similarity	17.7%	Pred. No.	0.0067:	
	Matches	122:	Conservative	283:	Mismatches 283; Indels 0; Gaps 0;
OY	145	GGAGAAAAAATGAAAAAGATTAAACATCATCAAAAATAGTTTCATAATTACATCATCTACTG	204		
Dd	1086	RKDDMDMTKMTWKDRADRRMAGDADBRMAWMDGAGTWTATATWWWWWMTATDTTWMDK	1027		
OY	205	ATTTCCTACTTATTTCCACTATCATCAAAAGTGACTCTTAAGAAGCATTTCGAATGTGTTAA	264		
Dd	1026	WWWATAAKTDITATWTWRTARBARWAGDRGCRDRRAATDADAGSRBDGRKKDKKD	967		
OY	265	AGTGATTTACTTTTATGATACACATATACTCCATATGATTAATAAGATPFGCAGGGTAAT	324		
Dd	966	RKDGDDDKKKKKKAARAAMWATKWMDWMDWDKMGDKKDKKADDDBDAGCKDDDK	907		
OY	325	TTTTCAACGACACACACATTTAAACATTGATCTACTAAAAATATAGAGGAAAAGCATATTAT	384		
Dd	906	GKDAADDPTDGRKDDDKDKMKMDMWKANGSTWGDATWAMAATDMMWGNADBDWMTWAAD	847		
OY	385	ATTAGTCCGCAAAATGCTCTTATGAGCGCTCTCAAAAATTTAAACAGATGATCATGTGCAT	444		
Dd	846	DMMADDRDWADMAWMDAMWAGATPADRBMGDRBAGRKGARKRRDRRADDKRDADDR	787		
OY	445	GTTTTGGATATTTTATATTTCTTAATTTCCACACCGGTGATCATCTATGAGGAAAT	504		
Dd	786	DDAATTTWTTTTRRDDDMRWKTDTWRWADPTWDDDDDDXRGATGGRKRRTWKR	727		
OY	505	ACGCCGTCTCAAAATAATTAAGTAATCATTAATTTGGGAAATCTATTTATTTTCGGA	564		
Dd	726	RWKRDPFTWMDADADPTARDRRRRGGDGAAGAGKTKGRRRRRDRATWMDRTAMWADA	667		
OY	565	GAATCTCAACGAACCTTAATAACAAGATTATCTTAGAAAAGATATFCGTAACCTTCCAG	624		
Dd	666	AAMTTTTDTDTDDMRKRBRRRKAGARRRRRTTARAAMDWMTWKAWMDAKWMDKTRADRMDRW	607		
OY	625	GAATTTGCTTAAATCAGAAATFACTTATGATATATTTAAATTTTAGACGCTACT	684		
Dd	606	AADTTWTDKRXDRWAKARARARARRDRARARADRRMTTKRTTATTTWTAARAAWAW	547		
OY	685	TCTCCTTTTGAACGCGCAGAAATGGAATTTGGCACAAAGATGGGAAACATGACGACATA	744		
Dd	546	WAMATTTATWTTTWTWTTTWTWTTTWTWTTTAAWMAAWMTWMAWTTAAANAAAAA	487		
OY	745	GACTTATTTGACTCACCAATGAAGGAGCTAGATCAGATATTTTGGCAAAATATPAAGAT	804		
Dd	486	AMAATTTTTTTTTTTTTAAWMAWMTWTTTWTWTTTAAWATTTTWTWTTWTTWMAAT	427		
OY	805	AATGAAATTATCATATGAGAACCTTTA	832		
Dd	426	ATTTTWTWTTTAAANAAAAAMWMTWTA	399		
RESULT 7					
	AL565455/c	LOCUS	1201 bp	mRNA	EST 12-MAY-2003
	DEFINITION	AL565455 Homo sapiens FETL BRAIN Homo sapiens cDNA clone			
	ACCESSION	CSDOF005YO18 3-PRIME, mRNA sequence.			
	VERSION	AL565455			
	KEYWORDS	AL565455.2 GI:30549492			
	SOURCE	EST.			
	ORGANISM	Homo sapiens (human)			
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
	REFERENCE	1 (bases 1 to 1201)			
	AUTHORS	Li,W.B., Gruber,C., Jesssee,J. and Polayes,D.			
	TITLE	Full-length cDNA libraries and normalization			
	JOURNAL	unpublished			
	COMMENT	On Feb 16, 2001 this sequence version replaced gi:12916848.			
		Contact: Genoscope			
		Genoscope - Centre National de Sequencage			
		BP 191 J1006 Evry cedex - France			
		Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr			

D	b		979	TATAMATTWNAATAAATWMNATANMATTTAATAAAADAATANMMWTMTTATTTTTTTT	920
Oy		224	ATCATCAAGTAGCTCTAGAACAACATTCGGAATGTAAAAGCATTACTTATGCAT	283	
D	b	919	TTTWTTTATWMTWWTTTATATW-----ATTMAAWAMAANAATWTATTTTTTTTATMAT	865	
OY		284	ACACTATACGCCCTTATGATATATTAAGATTCCAGGTAAATTTTCCAACGACACACAT	343	
D	b	864	MATTTTMATTTTTTTTTTWTATTTWTATTTWTATTTATTTATTTATTTTWTATTTWTAT	--t 808	
OY		344	TAAACATTGGATCTCAA AAAATATATAGAGGAAAACTATATATTTAGTCCGAAATGCTT	403	
D	b	807	TATTTWTTWTTTATTTTATWTTATWTTATWMTWWWMTAAWAATATATATMTATATATWT	748	
OY		404	ATGAGCGCTCGCAAAAATTTTAACGACATGATCATGTAGATGTTTGGAATTATTTATA	463	
D	b	747	WATTTWTTWTTTATTTTWTATTTTAATWTTATWATWATWTTWMAWTTTTTTTTTTTTT	688	
OY		464	TTCTTAATTCACACCGGTAGTACATCTATGAGAGATTAAGCGCTCTCAAAATATA	523	
D	b	687	TTTAAATTTATTTAATTATWMAAATAWNTATTTATAATWA-----TTAATTATTTAA	633	
OY		524	AAGTAAATCATAAATATATGGGAATCTATTTATTTGGGGAATCTCACAGAAC TTAA	583	
D	b	632	AATTTTATWMAAAAATATTTTTTTTATATTAATWAMATTTATATATATATWTTTAA	573	
OY		584	ATACAGATATATCTAGAAAAGATATCGTAAC TTTCCAGGAATTCAC TTAAATCA	643	
D	b	572	ATTWTTTATWATWTTATWTTTAAATTAATTTTTTTTTTATWATAAAMTAANAATWMMW	513	
OY		644	GAAATATACCTTATGATATATTAATAAATTTAT	675	
D	b	512	AAAAATWMMWTTTTTTTWTATWATAANAATTTWT	481	
RESULT 9					
ALJ36104/C			1201 bp mRNA linear EST 31-MAY-2003		
LOCUS			ALJ36104 Homo sapiens FETL BRAIN Homo sapiens cDNA clone		
DEFINITION			CSDP022YC18 5'-PRIME, mRNA sequence.		
ACCESION			ALJ36104		
VERSION			ALJ36104.2 GI:31260974		
KEYWORDS			EST.		
SOURCE			Homo sapiens (human)		
ORGANISM			Homo sapiens		
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
			Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE			1 (bases 1 to 1201)		
AUTHORS			L.J.W.B., Gruber,C., Jesssee,J. and Polayes,D.		
JOURNAL			Full-length CDNA libraries and normalization		
COMMENT			Unpublished		
			On Feb 13, 2001 this sequence version replaced gi:12795957.		
			Contact: Genoscope		
			Genoscope - Centre National de Sequencage		
			B.P 191 91006 Evry cedex - France		
			Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr		
			Llibrary was constructed by life technologies , a division of invitrogen . Contact : Feng Liang Email : fliange@life tech.com URL :		
			http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue genoscope sequence ID : CSDPF0Z2B809OP1.		
FEATURES					
source			location/Oualifiers		
			1..1201		

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DP022YC18"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: Brain; Vector: pCMVSPORT.6; 1st strand cDNA
was primed with a NotI-0130(OT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6

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BASE COUNT	359 a	119 c	146 g	409 t	168 others
ORIGIN	vector library was not normalized.				
Query Match	8.5%; Score 79.2; DB 9; Length 1201;				
Best Local Similarity	34.5%; Pred. No. 0.013;				
Matches	176; Conservative 99; Mismatches 228; Indels 7; Gaps 1;				
QY	50 AATCATTATTAATAATTCTTAATAAACAAGAAATCTGATTTTAACTACTTACTGCTATT 109				
DB	1161 WAAATATWTTTAAWAAWAAATWTAATATCAWAAWWTATWTTATTTTTTTTTTTTTTTWTA 1102				
QY	110 TCATGATATTCGACAGAGTAAATCATTTTAATTAAGAGAAWAAATATAAAGATTAACA 169				
DB	1101 YMAATATWTTWTTTAAWAAWWTWTTTAAWAAWWTWTTTAAWAAWWTWTTTAAWAAWWTW 1042				
QY	170 TCATCAAAATAGTTTTCATTAATTAACAGTCATGATTCTTACTTATTTACCTATCATC 229				
DB	1041 TTTTATWATASMTWAAWAAWAAWAAWAAWATWATWAAWATWTTWTTWTTTAAW 982				
QY	230 AAAGTGACOTCAAAAGACATTCGATGTAAAGGATTCCTTATGACATCACTA 289				
DB	981 TAAATTTTAAWAAWWTATTTATTAATATATTTTAAWAAWWTATTTAAWAAWWTAT 922				
QY	290 TAACTCCTTATGATTAATTAAGATTCAGGAGAAATTTTTCACACACACATTTAAACA 349				
DB	921 WAAATWTTWTTAAWAAWWTATTAATTAATAAATAAATAAATWTTT-----AAATTA 869				
QY	350 TTGATCTCAAAAATATATAGAGGAAAGACATTTATATAGTCCGAAATGCTTATAGAG 409				
DB	868 ATTTTATWAAWAAWAAWAAWAAWAAWTTTAAWAAWAAWAAWAAWAAWTTAAWTTATW 809				
QY	410 CCTCTCAAAAATTTAAACGAGATGATCATGATGATGTTTGGATTTTAAATATTTCTTA 469				
DB	808 ATTAATWAAWAAWAAWAAWAAWAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAAWTTAA 749				
QY	470 ATTCTCACACCGGTGAGTACATCTATGAGGAATTTACGCCCTCAAAATATATAAGTAA 529				
DB	748 WMTATATATWAAWAAWAAWAAWTTATATATTTTAAWAAWAAWAAWAAWAAWAAWAAW 689				
QY	530 ATCATTAATTTATGGGAATCTATTTATTTT 559				
DB	688 ATAAWAAATTTATATTAHAHTTATTTAAWAAW 659				
RESULT 10	CNS0021J 1101 bp DNA linear GSS 03-JUN-1999				
LOCUS	Drosophila melanogaster genome survey sequence TERN3 end of BAC #				
DEFINITION	BACR05N11 of RPO1-98 library from Drosophila melanogaster (fruit				
VERSION	fly), genomic survey sequence.				
ACCESSION	AL061936				
VERSION	AL061936.1 GI:4940214				
KEYWORDS	GSS.				
SOURCE	Drosophila melanogaster (fruit fly)				
ORGANISM	Drosophila melanogaster				
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
AUTHORS	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
TITLE	Ephyridoidae; Drosophilidae; Drosophila.				
JOURNAL	1 (bases 1 to 1101)				
COMMENT	Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a				

collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the *Drosophila melanogaster* genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP *Drosophila melanogaster* BAC library was prepared by Kazuo-ya Osoegawa and Aaron Mammone in Pieter de Jong's Laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, New York.

NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

```

1.1101
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR05N11"
/clone_lib="RPCI-98"
/note="end : TET3"
BASE COUNT      631 a      28 g      289 t      146 others
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Best Local Similarity 38.4%;  Pred. No. 0.02;
Matches 313;  Conservative 65;  Mismatches 431;  Indels 6;  Gaps 1;

35 AAAAACTAAATATTAATACATTTTAAATTTCTAATAACAGAAATCGATTTTAA 94
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
280 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 339
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
95 CTACTTACTGCTATTTCATGATTCCTGACGAGTAATACATTTAATTAAGAGAAAA 154
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
340 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 399
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
155 TGAAGAAGATTAACTCATCAAAATAGTTTCATATATACATCTACTGATTTTACTT 214
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
400 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 459
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215 ATTTCACCTATCATCAAGTGAAGTCTAAGAAAGACATTCGAAATGTAAGATTTAC 274
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
460 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 519
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275 TTTATGACATACCTATACCTCTTATGATTAATGAAGTTCAGGTAATTTTTCACGA 334
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
520 TTTATTTTWTWTATTAATTAATTTTATTTTATTTTATTTTATTTTAAATTAAMW 579
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335 CACACACATTAACATGATCTCAAAATATAGAGGAAGACATATATTTACTCCG 394
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
580 AATTTTATTAATAAATTTTAAATTTTAAATTAATAAATAAATTTTAAATTAATTT 639
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
395 AAATGCTTATGAGGCTCTCAAAATTTAAACGAGATGATCATGATGTTTGGAT 454
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
640 TTTTWTATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 699
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
455 TATTTTATATCTTAATTCACACCGGTGAGTCAATCTATGAGGAATTAAGCCTGCTC 514
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
700 AATTTTATTAATAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 759
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
515 AAAATTAATTAAGTAATCATTAATTTGGAATCTATTTATTTGCGAATAATCTCAC 574
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
760 TAAATTAATTAAT-----TAAATAATTTTAAATTTTAAATTTTAAATTTTAA 813
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575 AGAATTAATTAACAGATTAATTTCTAGAAAGATATCGTAATTTTCAGAGAAATGAT 634
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
814 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 873
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635 TTTAAATCAGAAATACCTTAATGATTAATTAATAATTTATGAGCTACTCTCTATG 694
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874 TTTAAATTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAAT 933
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934 KTAAKKKGGGTAAATDGTAAAGATTAATTAATTAATTAATTAATTAATTAATTA 993
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
755 ACTGACCAATGAAGGACTAGATCATATTTTTCGCAAAATTAAGATTAATTAATTA 814
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994 TAAAGAAATGAAGAAAGTGDATATTTTAAATTAATTAATTAATTAATTAATTA 1053
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QY 815 TCAATATGAAGACTTACTGATTTGATATTTAT 849
 Db 1054 GAAKAAARAKAAADAAAGATTDDAADAATATW 1088

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RESULT 11
LOCUS      CNS003BD      1101 bp      DNA      linear      GSS 03-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
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            fly), genomic survey sequence.
ACCESSION  AL064091
VERSION     AL064091.1  GI:4941847
KEYWORDS   GSS.
SOURCE      Drosophila melanogaster (fruit fly)
ORGANISM   Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
            1 (bases 1 to 1101)
            Genoscope.
            Direct Submission
            Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mamoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila\_bac.htm.
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BASE COUNT 395 a 120 c 103 g 334 t 149 others
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FEATURES

source

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Best Local Similarity 40.2%;  Pred. No. 0.031;
Matches 212;  Conservative 59;  Mismatches 254;  Indels 3;  Gaps 2;

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36 AAACTAAATATATATACATTTTAAATTTCTAATAAACAAGAAATCGATTTTAA 95
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565 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 624
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
96 TACTTACTGCTATTTCATGATTCCTGACGAGTA--TACATTTAATTAAGAGAAAA 153
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
625 TTTTATTTTATTTTATTTTATTTTAAATTAATTTTATTTTAAATTAATTTTAA 684
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
154 ATGAAAAAGATTAAATCATCAATATGTTTTCATTAATTTACAGTACATGATTTCTACT 213
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685 AAAAAAAAAAAAAAAAAAAAAAAAAAATTAATTAATTAATTAATTAATTAATTA 744
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214 TATTTACCTATCATCAAGTACTTAAGAGACATTTGAAATGTAAGATTAAGATTA 273
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745 TATTTTAAAAAATAATTTTATTTTATTTTAAATTAATTAATTAATTAATTAATTA 804
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274 CTTTATGACATACATTAATCTCTTATGATTAATTAAGATTTGACGAGTAATTTTCAACG 333
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Db
805 WTTTWTTAATTTWATAATTAAATTTTAAATTTTAAATTTAAAAAATA 864

OY
334 ACACACCATTAACATGTGATACCAAAAATATAGCGAACCTATTATAGTCC 393

Db
865 ATAAAAATTAATWTAATWATAAMTTTTAAATAAATTAAMTAAMAAAAAATTAAWTA 924

OY
394 GAAATGCTTAGTGAGGCCCTCAGAAAATTTAAACGAGATGCATGATGTTTGGGA 453

Db
925 AAAATWMAATMTTWTTTMTYTAAAAAWMYATTMAAMAMATATTTTATTTWATWATA 984

OY
454 TTATTTATATTCCTTAAT-TCTCACCGGAGATACATCATATGAGAGAATTAGCCGCG 512

Db
985 TAATAMWAAAAAAAAAATAAATTAATNNMAMAMWVAIAAANAIVCMMAAAAMWTATWYA 1044

OY
513 TCAAAATATATTAAGTAATCTATAATTTATGGGAAATCTATTATTTC 560

Db
1045 TAMAAAAAADAATATANNATTATTAANNAHNMAMWCATCTCCNCWC 1092

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RESULT 12
CONSNUMJ LOCUS DEFINITION
CN04NOJ 994 bp DNA linear GSS 01-SEP-2000
Tetradon nigroviridis genome survey sequence T7 end of clone
122P04 of library G from Tetradon nigroviridis genomic survey
sequence.
ACCESSION AL298972
AL298972 GI:8037822
GSS: genome survey sequence.
SOURCE Tetradon nigroviridis
Tetradon nigroviridis
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acinopterygii; Neopterygii; Teleostei; Euteleostei; Necteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontinae; Tetradon.
REFERENCE 1
AUTHORS Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PubMed 10835645
REFERENCE 2
AUTHORS Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PubMed 10899143
REFERENCE 3 (bases 1 to 994)
AUTHORS Genoscope.
REFERENCE Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequence :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetradon.
FEATURES
Source .
location/Qualifiers
1..994
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
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/clone_lib="G"
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BASE COUNT 543 a 49 c 36 g 194 t 172 others
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Best Local Similarity	43.58;	Pred. No. 0.036;		
Matches 263;	Conservative 25;	Mismatches 306;	Indels 10;	Gaps 2

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Db		391	AAATATANNAANAATAAAAAATAAAAAAMAAAATTTTATATATATATANMAATTNATATATAT	450
OY		76	ACAGAAATCTGATTTTTTAACACTACTGCTATTTTCATGTAATTCGTACGAGT----	A 130
Db		451	AAAAAAAAATATTTWAATTAATTAATTAATTAATTAATTTATATATATTAATAAATAAA	510
OY		131	ATCATATTAAATGAAGGAAAAAATNGAAAAAGATTAACATCATCAATAAATACTTGCTAA	190
Db		511	ATATATATATTAATTAATAAATAAATAATWMTATATTTATATATAMTPAATTTTATTAATA	570
OY		191	TTACAGTCATCTGATTTCTACTTATTTTCACCTATTCATCAAGAAGTACTTCAGAACACA	250
Db		571	ATAAAAAAAAAATNATAMNTAATATATAAATAATATATAAATAATMTTATATANMWTAAA	630
OY		251	TTTGCATGTAAAAAGCATTTACTTTATGTCATACACTATPATGCCCTTATGATTATAAG	310
Db		631	TATATATATWTTTATATATATATAAATAATNTATTTATATWATTTAAATTTTAAWTTTAA	690
OY		311	ATTCAGAGGTAAATTTTTCACAGCACACACATTAACATTAATGATATCAATAAATATGAG	370
Db		691	AAATATATAMNNAATATAMAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA	750
OY		371	GGAAGACTATTTATTTATGTTCCGAATGCTTATGAGCGCTTCAAAATTTTAAACGAG	430
Db		751	ATATATANNAANAATAAATTAATMAAATAAATAAATAATATATATATMAAATAAATAA	810
OY		431	ATGATCATGTAGAGTTTGTGATTA-----TTTATATCTCTTAATGTCACACGGGA	485
Db		811	ATATATATTTTANTMTAAATAAATAAATAAATAATATATTTTATTAATTAAMAATAATNTTA	870
OY		486	GTACATCTATGAGGAATTTACGCCCTGCTCAAATATATAAAGTAATCAATTAATTTGGG	545
Db		871	WTAAAAAANAATATANATTTATATATAAATAAAMATATATTTTGTAAAAATATTTTA	930
OY		546	AAATCTATTTTATTTCCGGAGAAATCCACACACACTTAATTAACAAGATTTATAGAAA	605
Db		931	AAAAAATTAATTTTAAAAATTTGTATTAATTTTATATATGAAAAATTTTAAAAAA	990
OY		606	GGAT 609	
Db		991	AAAW 994	
RESULT 13				
BX415878 1200 bp mRNA linear EST 15-MAY-2003				
DEFINITION LOCUS BX415878				
5-PRIME, mRNA sequence.				
ACCSSION BX415878				
VERSION BX415878.1 GI:30765550				
KEYWORDS EST.				
SOURCE Homo sapiens (human)				
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE 1 (bases 1 to 1200)				
AUTHORS Li,W.B., Gruber,C., Jesse,J. and Polayes,D.				
TITLE Full-length cDNA libraries and normalization				
JOURNAL Unpublished				
COMMENT Genoscope - Centre National de Sequencage				
BP 191 91006 EVRY cedex - France				
Email: sequef@genoscope.cns.fr, Web : www.genoscope.cns.fr				
Library was constructed by Life Technologies, a division of				
Invitrogen. Contact : Feng Liang Email : liliang@life tech.com URL :				
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600				

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